APPENDIX B SUBSTITUTE SHEETS



Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard	SEQ ID	Sequence	Binding
	1.	Peptide		-	Affinity
					(nM)
DRB1*0101	DR1	515.01	2128	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	2129	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	2130	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	2131	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	2132	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	2133	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	2134	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	2135	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	2136	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	2137	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	2138	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	2139	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2β1	507.02	2140	GRTQDENPVVHFFK	9.1
				NIVTPRTPPP	
DRB3*0101	DR52a	511	2141	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	2142	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2β2	553.01	2143	QYIKANSKFIGITE	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

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	DR5w12																														
	DR5w11	-0.0005				0.0340			0.0029	-0.0005		0.0080						0.7000					0.0540								
	DR4w15																														
	DR4w4	0.0830	-0.0022			0.8600			0.0930	0.0390	-0.0022	0.0260				-0.0022	-0.0022	5.6000					0.5600			-0.0022		-0.0022	-0.0022		
	DR3	0.0150				0.8900			0.2700	0.1400		0.0013		0.1300	0.0058			0.1300					0.0280				6,000	7400.0	0.005		•
ᆿ	DR2w81 DR2w282	-0.0007				0.0013			0.0024	-0.0007		0.0250						0.0095					0.0033								
CEA DR Super Motif Peptides with	OR2w81	0.6100 0.0110				2.5000 0.2300			0.3800	0.1600		0.0180						0.0830					0.0260 -0.0007								
r Motif P.	DRI	0.6100	-0.0004			2.5000			0.6200	0.3500	0.0011	0.0720				0.0009	0.0021	8.4000					0.0260			-0 0004		-0.0004	0.0210		
DR Supe	Position	120	29:	:8:	4X;	ಕರಿ:	×8	% =	86	88	፯፳	<u>2</u> 2	22	<u> </u>	126 127	<u>15</u>	4 <u>4</u> 5	22	262	218	នៃន	វត្ត	58.5 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8 7.8	2 28	283 284 287	30.5	310	325	375	33 32 32 32 32 32 32 32 32 32 32 32 32 3	392
	Exemplary SeqID Num	1815	1817	1820	25 1825 1825	1824	2 <u>2</u> 2	1827 1828	1829	1831	833 3433	1835 1836	1837 1838	1839 1840 1840	1841 1842	1843 1843	1845	1847	1849	1885 1885	1853	1855	1850	1858 1859	1860	1862	25.	9981	1868	6981 1870	1871
	Exemplary Sequence	RWCIPWORLLLTASL CIPWORLLTASLLT	WORLT.TASI.TFWN ORELLTASLLTFWNP	ASLLTFWNPPTTAKL	LTFWNPPTTAKLTIE	EVELEVHNEPOHEFG	YSWYKGERVDGNROI	NROIIGYVIGTOOAT GYVIGTOOATPGPAY	GPAYSGREIIYPNAS GREIIYPNASLLION	REIIYPNASI.I.JONI	NASLLIONIIONDTG ASLLIONIIONDTGF	IONIIONDTGFYTLH DTGFYTLHVIKSDLV	TGFYTI, HVIKSDI, VN FYTLHVIKSDL VNEE	TLHVIKSDL VNEEAT LHVIKSDL VNEEATG	KSDI, VNEFATGOFRV SDL VNEEATGOFRVY	OFR VYPEL PK PSISS YPEL PK PSISSNNSK	KPSISSNNSKPVEDK	YI, WWVNNOSI, PVSPR	NRTI,TI,FNVTRNDTA	ONPVSARRSDSVILN	LNVI,YGPDAPTISPL	APTISPLNTSYRSGE	OYSWFVNGTFOOSTO	TOELFIPNITVNNSG OFLFIPNITVNNSGS	ELFIPNITVNNSGSY IPNITVNNSGSYTCO	NITVNNSGSYTCOAH	RTTVTTITVYAEPPK	KPFITSNNSNPVEDE	SNPVEDEDAVALTCE NRTLTLLSVTRNDVG	LLSVTRNDVGPYECG RNDVGPYECGIONEL	ECGIONELSVDHSDP
	Core SeqID Num	1962 1963	1964	1961	1968	1970	1972 1973	1974 1975	1976	1978	1980	1982								8661	2000	2002 2002	2003 2004	200 5	2007	5005	2011	2012 2013	2014 2015	2016	2018
	Core	IPWORLLLT WORLLLTAS	LLLTASLLT LLTASLLTF	LTFWNPPTT	WNPPTTAKL	LLVHNLPOH	I.VHNI.POHI. YKGERVDGN	IIGYVIGTO IGTOOATPG	YSGREIIYP	IYPNASI I I	Trionilon	HONDTOFY FYTLHVIKS	YTI,HVIKSD	VIKSDLVNE IKSDLVNEE	LVNEEATGO	VYPELPKPS LPKPSISSN	ISSNNSKPV	WVNNOSI.PV	I.TI.FNVTRN	VSARRSDSV	LYGPDAPTI	YGPDAPTIS ISPLNTSYR	LSCHAASNP WFVNGTFOO	LFIPNITVN	SNINVLINGI	VNNSGSYTC	VTTITVYAE	VY AEPPK PF ITSNNSNPV	VEDEDAVAL.	VTRNDVGPY	IONELSVDH

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Table XIX
CEA DR Super Moil Peptides with
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	DR5w12																																			
	DR5w11										50000																	0.0016	0.0012							
	DR4w15																																			
	DR4w4								0.0180		0.0064		-0.0022						-0.0022					0.0037	0.0240		0.0270	1 8000	1.8000					•		
	DR3	0.0820	•								0.000	-								0.0037								0 1100	0.0750							
	DR2w81 DR2w282										0000	70000																70000	-0.0007							
0	DR2wB1										05000 0110	0.04.0																	0.0023							
	DRI								0.0005		0110	0.010	-0.0004						-0.0004					0.0820	0.1200		0.0240	0.0550	0.0640							
	Position	396 398	40	4 4	5	458	432	4 5	469	\$	- 64	56	497	75	55	558	23	282	287	888	89	019	55	679	638	639	653	654	99	699	129	889	33	2 <u>2</u>	252	3
	Exemplary SeqID Num	1872 1873	1874	1876	1877	929	1880	1881	1883	884	1882	2000	888	1889	681	1892	1893	1895	1896	1897	88	0061	1901	2062	905	506	1902	806	66	1161	1912	1914	1915	1916	8161	111
	Exemplary Sequence	ONELSVDHSDPVILN ELSVDHSDPVILNVL	SDPVII.NVI.YGPDDP	DPTISPSYTYYRPGV	SPSYTYYRPGVNLSL	RPGVNI SLSCHAASN	NI.SI.SCHAASNPPAO	YSWLIDGNIOOHTOE	OFLEISNITEKNSGL	ISNITEKNSGLYTCO	NSGL YTCOANNSASG	TITVSAELPKPSISS	SAFLPKPSISSNNSK	YLWWVNGOSLPVSPK	NRTI TLENVTRNDAR	I.FNVTRNDARAYVCG	VCGIONSVSANRSDP	CNSVSANKSDPVILD SOPVTI DVI VGPDTP	LDVLYGPOTPIISPP	DVLYGPDTPIISPPD	SCVI SGANI NI SCHS	NI,NI,SCHSASNPSPO	OYSWRINGIPOOHTO	INGIPOCHTOVLFIA	OVILFIAKITPNNNGT	VLFIAKITPNNNGTY	YACFVSNLATGRNNS	ACFVSNLATGRNNSI	NSIVK SITVSASGTS	VKSITVSASGTSPGL	SITVSASGTSPGLSA	TVGIMIGVI VGVALI	TAKLTIESTPFNVAE	VSWYKGERVICENKOI NOSLPVSPRLOLSNG	GENI, NI, SCHAASNPP	OCOLL VOI NEVENUA
	Core SeqID Num	2019	2021	2023	2024	202	2027	2028	670Z	2031	2032	2033	2035	2036	203 203 203 203	2039	2040	204 204	2043	2044	2045	2047	2048	2049	2021	2022	2054	2055	2020	2058	2029	2060	2062	2063 2064	2065	7000
	Core	LSVDHSDPV	VII.NVI.YGP	SPSYTYYR	YTYYRPGVN	VYRPGVNLS VNI SI SCHA	LSCHAASNP	LIDGNIOOH	FISNITER	ITEKNSGLY	LYTCOANNS	VKIII VSAE	I.PKPSISSN	WVNGOSLPV	VNGOSLPVS TI FNVTRN	VTRNDARAY	IONSVSANR	VSANRSDPV VTI DVI VGB	I VGPDTPII	YGPDTPIIS	ISPPINSSYI.	1.SCHSASNP	WRINGIPOO	POOHTOVL 1 ELAKITEN	FIAKITPNN	IAKITPNNN	FVSNLATGR	VSNLATGRN	VKSIIVSA	ITVSASGTS	VSASGTSPG	LSACAT VCI	LTIESTPFN	YKGERVIXGN	LNLSCHAAS	LPVSPRLUL

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PWQRLLLTA WQRLLLTA LLLTASLIT LLTASLTF LTASLTF LTEWNPT THEWNPTA WNPPTTA WNPTTA W	1962 1963 1964 1965		SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
WQRLLTA LLTASLLT LTASLLTF LTASLLTF TFWNPTT WNPPTTA WNPPTTA LTIESTPEN LYNNLPQH KGGRVDG GOYMGTQ GOYMGTQ GOYMGTQ GOYMGTQ TYPNASLL YPNASLLI YP	1963 1964 1965	RWCIPWQRLLLTASL	1815	0.0110	0.0700	-0.0004		
LLTASLLT LTASLLT LTASLLT LTASLLT TFWNPTT WNPPTTA LTIESTPEN LTHESTPEN LYPNACH GOYNGTO GOYNGTO GOYNGTO GOYNGTO GOYNGTO GOYNGTO TOWNSLLI YPNASLLI YPNASL	1964	CIPWQRLLLTASLLT	1816					
LITASLLIF LITASLLIF LITASLIF EWNPPTA WNPPTTAK LITESTPEN LITESTPEN LITESTPEN LYMNLPH YKGERVDG IGYVIGTQ GTQQATPG GTQQATPG GTQQATPG GTQQATPG GTQQATPG TYPNASLLI YPNASLLI YPNASLLI YPNASLLI YPNASLLI YPNASLLI YPNASLLI YPNASLLI	1965	WORLLTASLLTFW	1817					
TIASLLTF TIFWNPPTA WNPPTTA TIESTPEN TLLYHNLPQ VHNLPQ YKGEK VDG GTQQATPG GTQQATPG GTQQATPG GTQATPG TYPNASLL YPNASLLI		QRLLLTASLLTFWNP	1818		-0.0013			
TIEWNPPT WNPPTTA WNPPTTA TIESTPEN LIVHNLPQH KKGERVDG IGYVIGTQ GTQQATPG TSPNASLL YPNASLLI YPNASLL	1966	RLLLTASLLTFWNPP	1819					
WNPPTTA WNPPTTA WNPPTTA THESTPFN LLVHNLPQ LVHNLPQH KKGERVDG GTQQATPG GTQQATPG FSGREIYP TYPNASLL TYPNASLL TYPNASLLI TYPNASLLI TYPNASLLI TYPNASLLI TYPNASLLI	1961	ASLLTFWNPPTTAKL	1820					
WNPPTTAK TIESTPFN LLVHNLPQ VNNLPQH KYGEVDG GYQGATPG GYQGATPG SGREIIYP YPNASLL YPNASLLIQ PPNASLLIQ PPNASLLIQ	1968	LLTFWNPPTTAKLTI	1821					
LIVINLPQ LIVINLPQH KGERVDG GYVIGTQ GTQQATPG GYSGREIIYP YPNASLLI YPNASLLI YPNASLLI YPNASLLI YPNASLLI YPNASLLI YPNASLLI	1969	LTFWNPPTTAKLTIE	1822					
LVHNLPQ VHNLPQH KGERVDG IGYVICTQ GTQQATPG GTQQATPG GTQATPG TYPNASLLI PYPNASLLI PPNASLLIQ	1970	TAKLTIESTPFNVAE	1823					
VHNLPQH 'KGERVDG IGYVIGTQ GTQQATPG 'SGREIIYP IYPNASLLI PPNASLLI PPNASLLIQ	161	EVLLLVHNLPQHLFG	1824	3.4000	0.4100	0.1200		
'KGERVDG IGYVIGTQ GTQQATPG 'SGREIIYP IYPNASLLI YPNASLLI PNASLLIQ	1972	VLLLVHNLPQHLFGY	1825					
GYVIGTQ GTQQATPG SGREIIYP IYPNASLLI YPNASLLI PPNASLLIQ	1973	YSWYKGERVDGNRQ	1826					
GTQQATPG SGREIIYP IYPNASLL YPNASLLI PPNASLLIQ	1974	NROIIGYVIGTQQAT	1827					
SGREILYP IYPNASLL YPNASLLI PNASLLIQ	1975	GYVIGTQQATPGPAY	1828					
YPNASLL YPNASLLI PNASLLIQ	9261	GPAYSGREIIYPNAS	1829					
YPNASLLI PNASLLIQ	161	GREIIYPNASLLIQN	1830	1.2000	0.5600	0.0083		
PNASLLIQ	1978	REIIYPNASLLIQNI	1831					
NOINCI	1979	EIIYPNASLLIONII	1832	0.3100	0.1600	0.0029		
	1980	NASLLIONIIONDTG	1833		-0.0013			
CIONIOND	1861	ASLLIQNIIQNDTGF	1834					
HONDTGFY	1982	IONIIONDTGFYTLH	1835					
FYTLHVIKS	1983	DTGFYTLHVIKSDLV	1836	0.000	0.1100	0.0620		
YTLHVIKSD	1984	TGFYTLHVIKSDLVN	1837					
LHVIKSDLV	1985	FYTLHVIKSDLVNEE	1838					
VIKSDLVNE	9861	TLHVIKSDLVNEEAT	1839					
KSDLVNEE	1987	LHVIKSDLVNEEATG	1840					
LVNEEATG	1988	KSDLVNEEATGQFRV	1841					
VNEEATGO	6861	SDLVNEEATGQFRVY	1842					
VYPELPKP	1990	QFRVYPELPKPSISS	1843					
LPKPSISSN	1661	YPELPKPSISSNNSK	1844		-0.0013			
SSNNSKPV	1992	KPSISSNNSKPVEDK	1845		0.0033			
VEDKDAVA	1993	SKPVEDKDAVAFTCE	1846					
WVNNQSLP	1994	YLWWVNNQSLPVSP	1847	1.5000	0.6000	0.0460		
VNNQSLPV	1995	LWWVNNQSLPVSPR	1848		0.0082			
LTLFNVTR	9661	NRTLTLFNVTRNDTA	1849					
VTRNDTAS	1661	LFNVTRNDTASYKCE	1850					
VSARRSDS	8661	ONPVSARRSDSVILN	1821					
VILNVLYGP	6661	SDSVILNVLYGPDAP	1852					
,YGPDAPTI	2000	LNVLYGPDAPTISPL	1853					
YGPDAPTIS	2001	NVLYGPDAPTISPLN	1854					
SPLNTSYR	2002	APTISPLNTSYRSGE	1855					
LSCHAASN	2003	NLNLSCHAASNPPAQ	1856		1			
WFVNGTFQ	2004	QYSWFVNGTFQQST	1857	90000	0.0270	0.0039		
LFIPNITVN	2002	TQELFIPNITVNNSG	1858					
FIPNITVNN	2006	OELFIPNITVNNSGS	1829					
IPNITVNNS	2007	ELFIPNITVNNSGSY	1860					



CEA DR Super Motif Peptides with Binding

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Sequence Se	SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
TVNNSGSY	2008	IPNITVNNSGSYTCQ	1981					
VNNSGSYT	2009	NITVNNSGSYTCQAH	1862					
LNRTTVTTI	2010	DTGLNRTTVTTITVY	1863		0.0088			
VTTITVYAE	2011	RTTVTFITVYAEPPK	1864					
VYAEPPKP	2012	TITVYAEPPKPFITS	1865					
TSNNSNPV	2013	KPFITSNNSNPVEDE	1866		-0.0013			
VEDEDAVA	2014	SNPVEDEDAVALTCE	1867					
LTLLSVTR	2015	NRTLTLLSVTRNDVG	1868		0.0021			
VTRNDVGP	2016	LLSVTRNDVGPYECG	1869					
VGPYECGI	2017	RNDVGPYECGIQNEL	1870					
QNELSVDH	2018	ECCIONELSVDHSDP	1871					
SVDHSDP	2019	ONELS VDHSDPVILN	1872					
VDHSDPVIL	2020	ELSVDHSDPVILNVL	1873					
VILNVLYGP	2021	SDPVILNVLYGPDDP	1874					
YGPDDPTIS	2022	NVLYGPDDPTISPSY	1875					
SPSYTYYR	2023	DPTISPSYTYYRPGV	1876					
YTYYRPGV	2024	SPSYTYYRPGVNLSL	1877					
YYRPGVNL	2025	SYTYYRPGVNLSLSC	1878					
WNLSLSCH	2026	RPGVNLSLSCHAASN	1879					
SCHAASN	2027	NLSLSCHAASNPPAQ	1880					
LIDGNIQQH	2028	YSWLIDGNIQQHTQE	1881					
FISNITEK	2029	TQELFISNITEKNSG	1882					
FISNITEKN	2030	QELFISNITEKNSGL	1883		-0.0013			
TEKNSGLY	2031	ISNITEKNSGL YTCQ	1884					
LYTCQANN	2032	NSGLYTCQANNSAS	1885					
VKTITVSAE	2033	RTTVKTITVSAELPK	9881	0.0050	0.020	-0.004		
VSAELPKP	2034	TITVSAELPKPSISS	1887					
PKPSISSN	2035	SAELPKPSISSNNSK	888		0.0013			
WVNGQSLP	2036	YLWWVNGQSLPVSP	1889					
VNGQSLPV	2037	LWWVNGQSLPVSPR	1890					
LTLFNVTR	2038	NRTLTLFNVTRNDAR	1881					
VIKNDAKA	6502	LENVIKNDAKAT VC	1807					
IQNSVSAN	2040	ONEVICANIPEDRATION	6691					
VSAINKSDF	100	TURNING TAND	1864					
VGPDTPII	2043	LOVEVGPOTPHSPP	1896		-0.0013			
KGPDTPHS	2044	DVLYGPDTPIISPPD	1897					
SPPDSSYL	2045	TPIISPPDSSYLSGA	1898					
SGANLNL	2046	SSYLSGANLNLSCHS	6681					
SCHSASN	2047	NLNLSCHSASNPSPQ	1900					
WRINGIPQQ	2048	QYSWRINGIPQQHTQ	1901					
POOHTOVL	2049	INGIPQQHTQVLFIA	1902					
LFIAKITPN	2050	TQVLFIAKITPNNNG	1903		0.0038			
FIAKITPNN	2051	QVLFIAKITPNNNGT	1904		0.0024			
AKITPNNN	2052	VLFIAKITPNNNGTY	1905					
VACEVENI	2062	STA INSVIOUNT ATOM	1906					

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	Table XIX		CEA DR Super Motif Peptides with Binding	Peptides wi	ith Bindin	<u>₽</u>		
Core	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19 DR7	DR7	DR8w2	DR9	DRw53
FVSNLATG	2054	YACFVSNLATGRNN	1907		0.0070			
VSNLATGR	2055	ACFVSNLATGRNNSI	8061					
IVKSITVSA	2056	NNSIVKSITVSASGT	1909	0.0690	0.0370	0.0120		
VKSITVSAS	2057	NSIVKSłTVSASGTS	1910	0.0460	0.0760	0.0170		
ITVSASGTS	2058	VKSITVSASGTSPGL	1161			•		
VSASGTSP	2059	SITVSASGTSPGLSA	1912					
LSAGATVGI	2060	SPGLSAGATVGIMIG	1913					
IMIGVLVGV	2061	TVGIMIGVLVGVALI	1914					
LTIESTPFN	2062	TAKLTIESTPFNVAE	1915					
YKGERVDG	2063	YSWYKGERVDGNRQ	9161					
LPVSPRLO	2064	NOSLPVSPRLQLSNG	1917					
LNLSCHAA	2065	GENLNLSCHAASNPP	1918					
LPVSPRLO	2066	GOSLPVSPRLQLSNG	1919					

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	DR5w12								-										
	DR4w4 DR4w15 DR5w11 DR5w12	-0.0008																	
	DR4w15																		
	DR4w4	0.3200 -0.0055	_								_	_		_					_
	DR3	0.3200	0.1300	0.0058	•	•	•	•	•	0.0042	0.0054	0.0039	•	0.0820	•	•	•	•	0.0037
CEA DR 3a Motif Peptides with Binding	DR2w281 DR2w282 DR3	0.0044 0.0105 -																	
ptides w	DRI	0.004																	
a Motif Pe	Position	110	122	126	127	137	162	210	232	315	332	340	392	396	410	493	\$18	282	288
CEA DR 3	Exemplary SeqID Num	1920	1921	1922	1923	1924	1925	1926	1927	1928	1929	1930	1631	1932	1933	1934	1935	1936	1937
Table XXa	Exemplary Sequence	QNIIQNDTGFYTLHV	LHVIKSDLVNEEATG	KSDL VNEEATGQFRV	SDLVNEEATGQFRVY	QFRVYPELPKPSISS	AVAFTCEPETQDATY	TASYKCETQNPVSAR	NVLYGPDAPTISPLN	TITVYAEPPKPFITS	SNPVEDEDAVALTCE	AVALTCEPEIQNTTY	ECGIONELSVDHSDP	ONELSVDHSDPVILN	NVLYGPDDPTISPSY	TITVSAELPKPSISS	AVAFTCEPEAQNTTY	SDPVTLDVLYGPDTP	DVLYGPDTPIISPPD
	Core Exemplar SeqID Num Sequence	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084
	Core	IONDTGFYT	IKSDLVNEE	LVNEEATGO	VNEEATGOF	VYPELPKPS	FTCEPETQD	YKCETONPV	YGPDAPTIS	VYAEPPKPF	VEDEDAVAL	LTCEPEION	IONELSVDH	LSVDHSDPV	YGPDDPTIS	VSAELPKPS	FTCEPEAON	VTLDVLYGP	YGPDTPIIS

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		Table XXa	CEA DR 3a Motif Peptides with Binding Data	otif Peptide	s with Bir	ading Data		
Core Sequence	Core Exemplar SeqID Num Sequence	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
IONDTGFYT	2067	QNIIQNDTGFYTLHV	1920	0.3600	-0.0017	-0.000		
IKSDL VNEE	2068	LHVIKSDLVNEEATG	1921					
LVNEEATGQ	5069	KSDLVNEEATGQFRV	1922					
VNEEATGOF	2070	SDLVNEEATGQFRVY	1923					
VYPELPKPS	2071	QFRVYPELPKPSISS	1924					
FTCEPETQD	2072	AVAFTCEPETQDATY	1925					
YKCETONPV	2073	TASYKCETQNPVSAR	1926					
YGPDAPTIS	2074	NVLYGPDAPTISPLN	1927					
VYAEPPKPF	2075	TITVYAEPPKPFITS	1928					
VEDEDAVAL	2076	SNPVEDEDAVALTCE	1929					
LTCEPEION	2077	AVALTCEPEIQNTTY	1930					
IONELSVDH	2078	ECCIONELSVDHSDP	1831					
LSVDHSDPV	2079	ONELSVDHSDPVILN	1932					
YGPDDPTIS	2080	NVLYGPDDPTISPSY	1933					
VSAELPKPS	2081	TITVSAELPKPSISS	1934					
FTCEPEAON	2082	AVAFTCEPEAQNTTY	1935					
VTLDVLYGP	2083	SDPVTLDVLYGPDTP	1936					
YGPDTPIIS	2084	DVLYGPDTPIISPPD	1937					

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Core Core Examplary Position DR I DR 2.201 DR 2.202 DR 3.201 DR 4.401 DR 5.401 DR 5.401 DR 2.202 DR 3.202 DR 4.401 DR 5.401 DR 5.4				Table XXb		CEA D	R 3b Motif P	CEA DR 3b Motif Peptides with Binding Data	Binding l)ata			
2085 NEEATGOFR VYPELP 1938 131 -0.00027 2086 ISPLINTSYRSGENLN 1939 242 -0.00027 2088 SGSYTCOAHUSDTGL 1940 224 -0.00027 2088 RIQLSNDNRTLTLS 1941 368 0.0001 -0.0007 0.2200 2090 GANLALSCHAASAPP 1943 430 -0.0007 -0.0055 -0.0055 2091 GANLALSCHAASAPP 1944 608 -0.0007 -0.0057 -0.0055 2092 RLPASPETHLDMIRH 1945 84 -0.0007 -0.0027 -0.0027 2093 VLLAHNOYRQVEQR 1946 84 -0.0001 -0.0009 0.3100 -0.0055 2094 ALTILDTMSRACHP 1948 465 0.0140 0.0199 0.0027 -0.0027 2095 LALIHNYTHLCFVHT 1948 465 0.0140 0.0190 0.0035 2095 CALIHNYTHLCFVHT 1948 462 0.0016 -0.0007 0.0025 2095	Core	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DRI	DR2:w281	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12
2086 ISPINITSYRSGENLN 1939 242 -0.00027 2087 SGSYTZOAHINSDTGL 1940 234 -0.00027 2088 NGSPLYSPRLQLSND 1941 360 -0.0007 -0.0007 2089 RLQLSNDNRTLTLLS 1942 368 0.0001 -0.0007 -0.0007 2091 GANLALSCHAASNP 1943 430 -0.0007 -0.0007 -0.0027 2091 GANLALSCHAASNP 1944 608 -0.0007 -0.0007 -0.0007 2092 RLADAROVROPROPR 1944 84 -0.0007 -0.0007 -0.0007 2093 VLAJHNOVROPROPR 1946 84 -0.0001 0.0029 0.0029 2094 ALJHNYRLCPWHT 1948 465 0.0140 0.0099 0.3100 -0.0027 2095 LALJHNYRLCPWHT 1948 465 0.0145 -0.0007 0.0029 2094 GWAYLEDVRLVRELYH 1948 465 0.0145 -0.0007 0.0005 2100 G	ATGOFRVYP	2085	NEEATGOFRVYPELP	1938	131				-0.0027				
2081 SGSYTCQAHNSDTGL 1940 294 -0.00027 2088 NQSLPVSPRLQLSND 1941 366 -0.0001 -0.0001 2089 RLQLSUDNITLLS 1942 368 0.0001 -0.0007 -0.0053 2090 GVANLALSCHAASNPP 1943 430 -0.0007 -0.0027 -0.0027 2091 RLPASPETHLDMLRH 1945 34 608 -0.0007 -0.0027 2093 VLIAHNQVRQVPLQR 1946 84 -0.0001 -0.0007 -0.0027 2094 ALTLIDTNRSRACHP 1947 180 -0.0015 -0.0007 -0.0027 2095 VLAHNTHLCPVHT 1948 463 0.0140 0.0199 0.0100 -0.0055 2094 VLALIHANTHLCPVHT 1948 483 -0.0001 0.0105 -0.0007 2095 VLALIHANTHLCPVHT 1941 483 -0.0001 0.0105 -0.0007 2096 MSYLEDVRLYHER 1951 832 0.0004 -0.0009 0.0105 <td>LNTSYRSGE</td> <td>2086</td> <td>ISPLNTSYRSGENLN</td> <td>1939</td> <td>242</td> <td></td> <td></td> <td></td> <td>-0.0027</td> <td></td> <td></td> <td></td> <td></td>	LNTSYRSGE	2086	ISPLNTSYRSGENLN	1939	242				-0.0027				
2088 NGSLPVSFRLQLSND 1941 360 0.0071 2089 RLQLSNDNRTLTLLS 1942 368 0.0001 -0.0007 0.0035 2090 GYNLSLSCHAASNP 1943 430 -0.0007 -0.0007 0.0035 2091 GANLNLSCHAASNPS 1944 608 -0.0007 -0.0027 -0.0027 2093 VLJAHNAPLCHAR 1946 84 -0.001 -0.0027 -0.0027 2094 ALTLIDTNRSRACHP 1948 84 -0.001 0.0099 0.0009 0.0330 2094 ALTLIDTNRSRACHP 1948 465 0.0140 0.0999 0.0009 0.0355 2094 ALTLIDTNRSRACHPHOALLH 1948 482 -0.0001 0.0005 0.0055 2094 ALTLIDTNRSRACHPHOALLH 1949 482 -0.0001 0.0005 0.0055 2098 GMSYLEDVRLVHRDL 1951 832 0.0001 0.0100 0.0055 2100 CVMIDSECRPRFEL 1954 104 0.0006	YTCOAHNSD	2087	SGSYTCQAHNSDTGL	1940	294				-0.0027				
2089 RLQLSNDNRTLTLLS 1942 368 0.0001 -0.0005 -0.0055 2090 GYNLSLSCHAASNPR 1941 430 -0.0001 -0.0007 0.0075 2091 GANLNISCHSANPR 1944 608 -0.0007 -0.0007 2093 VLJAHOVROVROR 1946 84 -0.0007 -0.0007 2094 ALTLIDTNRSRACHP 1947 180 -0.0001 0.0130 0.0230 2095 ALTLIDTNRSRACHP 1948 465 0.0140 0.0009 0.0009 0.0005 2094 ALTLIDTNRSRACHP 1948 482 -0.0001 0.0105 -0.0007 -0.0055 2095 WDQLFRIPHTALLT 1949 482 -0.0001 0.0105 -0.0005 -0.0055 2099 CWMIDSECRPRFIEL 1952 938 0.0015 -0.0005 -0.0025 2100 CWMIDSECRPRFIEL 1954 104 -0.0005 -0.0005 -0.0005 2101 CKAAPQPIPPPARS 1954 104 <	LPVSPRLQL	2088	NOSLPVSPRLQLSND	1941	360				0.0071				
2090 GVNLSLSCHAASNPP 1943 430 0.0073 2091 GANLNISCHEASNPR 1944 608 -0.0027 2092 RLPASPETHLDMLRH 1945 34 -0.0027 2093 VLIAHINOYROVELQR 1946 84 -0.0020 2094 ALTLIDTNRSRACHP 1947 180 0.0350 2095 ALTLIDTNRSRACHP 1947 180 0.0009 0.0009 2095 ALTLIDTNRSRACHP 1947 182 -0.0001 0.0009 0.0350 2096 ALTLIDTNRSRACHP 1948 452 0.0001 0.0005 0.0005 2095 LALIHHYTHLCFWHT 1948 452 0.0001 0.0005 0.0005 2099 GWASYLEDNRLVHRDL 1951 82 0.0015 -0.0007 0.0005 2100 GGGAARQPHPPARS 1954 104 0.0006 0.0150 0.0005 2101 GGGAARQPHPPARS 1954 294 0.0006 0.0150 0.0005 2102	LSNDNRTLT	2089	RLQLSNDNRTLTLLS	1942	368	0.0001		-0.0007	0.3200	-0.0055		-0.0008	
2091 GANLINLSCHSASNPS 1944 608 -0.0022 2092 RLPASPETHLDMIKH 1945 34 -0.0027 2093 VLIAHNOVROVEQRE 1946 84 0.0290 2094 A.TLIDTNRSRACHP 1947 180 0.0350 2095 A.LJHHNTHLCFVHT 1948 465 0.0140 0.0990 0.0009 0.3100 2096 WDOLFKNHPHOALLHT 1949 482 -0.0001 0.0015 -0.0007 0.0005 2097 HSCVDLDDKGCPREQ 1951 812 -0.0001 0.0150 -0.0005 -0.0055 2099 CWMIDSECRPREREL 1952 958 0.0036 -0.0006 0.0150 -0.0055 2100 GGGAAPQPHPPAFS 1953 1200 -0.0006 0.0150 -0.0025 2101 HCACALSKVAELVH 1954 290 -0.0006 0.0150 -0.0025 2101 HCACALSKVAELVH 1954 290 -0.0006 -0.0010 0.0025 2104 HCALSKVAELYDH	LSLSCHAAS	2090	GVNLSLSCHAASNPP	1943	430				0.0075				
2092 RLPASPETHLDMLRH 1945 34 -0.0027 2093 VULAHNOVROVPLQR 1946 84 -0.0027 2094 ALTLIDTNSRACHP 1947 180 0.0350 2095 ALLIHHYTHLCPUT 1948 465 0.0140 0.0990 0.0009 0.3100 2096 WDOLFRUHQALLHT 1948 482 -0.0001 0.0015 -0.0007 0.0055 2097 HSCVDLDDKGCPAEQ 1950 632 -0.0001 0.0150 0.0005 2099 GMSYLEDVRLVHRDL 1951 832 -0.0006 0.0150 0.0037 2099 GMSYLEDVRLVHRDL 1951 1200 -0.0066 0.0150 0.0053 2109 GMSYLEDVRLVHRDL 1951 1200 -0.0066 0.0150 0.0035 2101 WX-LHTTKJGGEPH 1955 234 104 -0.0016 -0.0015 -0.0025 2103 TLKIGGEPHISYPEL 1956 290 -0.0006 -0.0010 0.0025 2104	LNLSCHSAS	1007	GANLNLSCHSASNPS	1944	809				-0.0027				
2093 VLIAHNQVRQVPLQR 1946 84 0.0290 2094 ALTLIDTNISSRACHP 1947 180 0.0350 0.0350 2095 LALIHHNTHLCFVHT 1948 463 0.0140 0.0990 0.0009 0.3100 -0.0055 2096 WDQLFRNPHQALLHT 1949 482 -0.0001 0.0150 -0.0005 -0.0055 2097 HSCVDLDDKGCPAEQ 1950 632 -0.0001 0.0150 -0.0055 2099 CWMIDSECRERFREL 1951 83 0.0366 -0.0006 0.0150 -0.0055 2100 CVAMIDSECRERFREL 1951 1200 -0.0006 0.0150 -0.0055 2100 CVAMIDSECRERFREL 1954 104 0.0005 -0.0025 -0.0025 2101 EFQAAISKLAVELYH 1954 104 -0.0006 -0.0015 -0.0025 2103 TLKIGGEPHISYPL 1956 290 -0.0006 -0.0015 -0.0025 2104 MAIYKGSQHMTEVAL 1954 104	ASPETHLDM	2092	RLPASPETHLDMLRH	1945	34				-0.0027				
2094 ALTLIDTNRSRACHP 1947 180 0.0330 2095 LALLHHYTHICKPHT 1948 465 0.0140 0.0090 0.0035 2096 WDQLFRNPHALLHT 1949 482 -0.0001 -0.0007 -0.0005 2097 HSCVLDDKGCFARG 1950 632 -0.0001 -0.0007 -0.0055 2099 CWMIDSECRPRFIEL 1952 938 0.0036 -0.0006 0.1800 -0.0055 2100 QGGAAPQPHPPAFS 1933 1200 -0.0006 0.0150 0.4800 2101 FFQAARKWHELT 1954 104 -0.0005 -0.0025 2102 VKVLHITKIGGEPH 1955 290 -0.0006 -0.0010 -0.0025 2103 TLKIGGEPHISYPL 1956 290 -0.0006 -0.0010 -0.0025 2104 EFQAALSKKALTQH 1958 233 0.0003 -0.0005 -0.0025 2104 MAIYKQSQHMTEVYR 1959 160 -0.0010 -0.0010 -0.0025	AHNOVROVP		VLIAHNQVRQVPLQR	1946	84				0.0290				
2095 LALIHHYTHLCFVHT 1948 465 0.0140 0.0990 0.0009 0.3100 -0.0055 2096 WDOLFRNHQALLHT 1949 482 -0.0001 0.0015 -0.0007 0.0035 2099 CWMIDSECRPRELE 1951 832 -0.0006 -0.0150 0.1800 2099 CWMIDSECRPREREL 1952 948 0.0036 -0.0006 0.0150 0.4500 2100 CGGAAPQHIPPAFS 1933 1200 0.0036 -0.0036 0.0035 2101 EGAALSIKWAELVH 1954 290 2003 -0.0035 2103 TLKIGGEBHISYPL 1956 290 -0.0036 -0.0010 0.0035 2104 EFQAALSIKWAELVH 1957 104 -0.0006 -0.0010 0.0035 2105 ERSILGDPRKLLTQH 1958 236 0.0006 -0.0010 0.0035 2104 EFQAALSIKWAELVH 1957 104 0.0006 -0.0010 0.0003 2105 ERSILGDPRKLLTQH <t< td=""><td>LIDTNRSRA</td><td></td><td>ALTLIDTNRSRACHP</td><td>1947</td><td>180</td><td></td><td></td><td></td><td>0.0350</td><td></td><td></td><td></td><td></td></t<>	LIDTNRSRA		ALTLIDTNRSRACHP	1947	180				0.0350				
2096 WDQLFRNPHQALLHT 1949 482 -0.0001 0.0015 -0.0007 0.9000 -0.0055 1 2098 GAXYLEDPRLZHRIZ 1951 832 -0.0016 -0.0007 -0.0027 1 2099 CWMIDSECRPRFEL 1951 1958 0.0036 -0.0006 0.0150 -0.0055 2 1009 CWMIDSECRPRFEL 1951 1200 -0.0006 0.0150 0.4500 -0.0055 2 1001 EFQAALSRKAPELM 1954 104 -0.0005 -0.0023 -0.0023 2 102 VKVLHITLKIGGEPH 1955 284 -0.0006 -0.0019 -0.0023 2 103 TLKIGGEPHISYPL 1956 290 -0.0006 -0.0010 0.0023 2 104 EFQAALSRKVARLTQH 1958 23 0.0003 -0.0016 -0.0023 2 104 EFQAALSRKVARLTQH 1958 23 0.0003 -0.0006 -0.0010 0.0023 2 104 EFQAALSRKVARLTQH 1958 210 0.0003 -0.0006 -0.0010	HHNTHLCF	2095	LALIHHNTHLCFVHT	1948	465	0.0140	0.0990	6000.0	0.3100	-0.0055		0.0025	
p 1997 HSCVDLDDKGCPAEQ 1950 632 -0.0027 1 2098 GMSYLEDYRLVHRDL 1931 832 -0.0006 0.0150 0.1800 2099 CWMIDSECRPREEL 1952 958 0.0036 -0.0006 0.0150 0.0035 2100 CWADARGHAPPAFE 1953 1200 -0.0005 -0.0035 2101 EFQAALSRKWEELH 1954 104 -0.0035 2102 VKVLHITLKIGGEPH 1956 290 -0.0035 2103 TLKIGGEPHISYPL 1954 104 -0.0035 2104 EFQAALSRKVAELTQH 1958 235 0.0006 -0.0010 0.0025 2105 EDSILGOPKKLITQH 1958 235 0.0006 -0.0010 0.0025 2104 EFOALSRKVEYLDD 1960 194 -0.0025 -0.0025 2105 LINYEGKIMTEVYR 1958 160 -0.0010 0.0025 2108 GEYFTLQIRGRERFE 1961 194 0.0290	LFRNPHQAL	2096	WDQLFRNPHQALLHT	1949	482	-0.0001	0.0015	-0.0007	0.9000	-0.0055		*0000	
1.098 GMSYLEDVRLVHRDL 1951 832 0.1800 0.1800 0.1800 0.0990 CWMIDSECREFREL 1952 958 0.0036 -0.0006 0.0150 0.0025 0.002	VDLDDKGCP	2097	HSCVDLDDKGCPAEQ	1950	632				-0.0027				
2099 CWMIDSECRPREEL 1952 938 0.0036 -0.0006 0.0150 0.4300 -0.0055 2100 QGCAAPQPHPPAFS 1933 1200 -0.0036 -0.0035 -0.0035 2101 FFQAAISRAWELVH 1954 104 0.0039 -0.0035 2102 VKVLHFILKIGEPH 1954 290 -0.0035 -0.0035 2103 TLKIGGEPHISYPPL 1956 290 -0.0010 -0.0025 2103 EFQAALSRKVAELVH 1958 235 0.0003 -0.0010 -0.0010 2104 EFQAALSRKVAELVH 1958 235 0.0003 -0.0010 0.0035 E 2104 MAIYCQCHMTEVYR 1958 160 -0.0010 -0.0035 7 2107 LIRVEGKLKYREYLD 1960 194 0.0320 7 2107 LIRVEGKLKYREYEF 1961 325 0.0003 -0.0010	YLEDVRLVH	2098	GMSYLEDVRLVHRDL	1951	832				0.1800				
2100 QGGAAPQPHPPAFS 1933 1200 -0.0023 . 2101 EFQAAJSRKNYELVH 1934 104 0.0039 . 2102 VKVLHTIKIGGEPH 1935 284 -0.0035 . 2103 TLKIGGEPHISYPPL 1936 290 -0.0025 . 2104 EFQAALSRKVAELVH 1937 104 0.0027 . 2105 EOSILGOPPKLLTQH 1938 233 0.0003 -0.0010 0.0003 . 2105 MAIYKOSQHMTEVVR 1959 160 -0.0010 0.0025 . 2107 LIRYEGKLKYEYLDD 1960 194 0.0930 . 2107 LIRYEGKLKYEYLE 1961 325 0.0220	IDSECRPRF	2099	CWMIDSECRPRFREL	1952	988	0.0036	-0.0006	0.0150	0.4500	-0.0055		8000°O-	
2101 EFQAAISRKMVELVH 1954 104 0.0039 2102 VKVLHHTLKIGGEPH 1955 284 -0.0023 2103 VKVLHHTLKIGGEPH 1955 290 -0.0023 2104 EFQAALSRKVASPYL 1957 104 0.0023 2105 EDSILGDPKKLLTQH 1958 235 0.0003 -0.0010 0.6700 2 2106 MAIYKQSQHATEVR 1959 160 -0.0025 -0.0025 2 107 LIRVEGNLRVEYLDD 1960 194 0.0930 2 108 GEYFTLQIRGRERFE 1961 325 0.0290	AAPQPHPPP	2100	QGGAAPQPHPPAFS	1953	1200				-0.0025				
102 VKVLHHTLKIGGEPH 1955 284 -0.0023 2103 TLKIGGEPHISYPPL 1956 290 -0.0023 E 2104 EPQAALSRX VAELVH 1957 104 0.0027 . 2105 EDSILGOPKKLLTQH 1958 235 0.0003 -0.0016 -0.0010 0.5700 re 2106 MAIYKQSQHMTEVR 1959 160 -0.0025 -0.0025 re 2107 LIRVEGNIRARYENLD 1960 194 0.0930 re 2108 GEYFTLQIRGRERFE 1961 325 0.0290	AAISRKMVE	2101	EFQAAISRKMVELVH	1954	104				0.0039				
2103 TLKIGGEPHISYPPL 1956 290 -0.0023 E 2104 EPGAALSRKVAELVH 1957 104 0.0027 0.0027 2 2105 EDSILGDPKKLITQH 1958 235 0.0003 -0.0006 -0.0010 0.00055 FE 2106 MAIYKQSQHMTEVR IP39 160 -0.0006 -0.0010 0.0025 F 2107 LIRVEGNIRARPIDD 1960 194 0.0930 E 2108 GEYFTLQIRGRERFE 1961 325 0.0290	LHHTLKIGG	2102	VKVLHHTLKIGGEPH	1955	284				-0.0025				
E 2104 EFQAALSRKVAELVH 1957 104 0022 2. 2105 EDSILGOPKKLITQH 1958 235 0.0003 -0.0006 0.0010 0.00055 FE 2106 MAIYKQSQHMTEVR 1959 160 0.0023 -0.0025 2. 2108 GEYTILQIRGRERFE 1961 325 0.0003 0.0290	IGGEPHISY	2103	TLKIGGEPHISYPPL	1956	290				-0.0025				
2105 EDSILGDPKKLLTQH 1958 235 0.0003 -0.3006 -0.0010 0.6700 -0.0055 E 2106 MAIYKQSQHMTEVYR 1959 160 -0.0025 -0.0025 ? 2107 LIRVEGNLRVEYLDD 1960 194 0.0930 2108 GEYFTLQIRGRERFE 1961 325 0.0290	AALSRKVAE	2104	EFQAALSRKVAELVH	1957	104				0.0027				
E 2106 MAIYKQSQHMTEVVR 1959 160 7 2107 LIRVEGNLRVEYLDD 1960 194 2108 GEYFTLQIRGRERFE 1961 325	ILGDPKKLL	2105	EDSILGDPKKLLTQH	1958	235	0.0003	-0,000	-0.0010	0.6700	-0.0055		-0.0008	
7 2107 LIRVEGNLRVEYLDD 1960 194 (2108 GEYFTLQIRGRERFE 1961 325	YKQSQHMTE	2106	MAIYKQSQHMTEVVR	1959	160				-0.0025				
2108 GEYFTLQIRGRERFE 1961 325	VEGNLRVEY	2107	LIRVEGNLRVEYLDD	1960	194				0.0930				
	FTLQIRGRE	2108	GEYFTLQIRGRERFE	1961	325				0.0290				

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			CEA DR 3b Motif Peptides with Binding Data	with Binding Data			
Jore Sequence .	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9
ATCOEDVVD	2086	NEE & TGOER VYDE! P	1018				
NTSYRGE	2086	ISPINISYRSGENLN	1939				
YTCOAHNSD	2087	SGSYTCOAHNSDTGL	1940				
LPVSPRLOL	2088	NOSLPVSPRLQLSND	1941				
LSNDNRTLT	2089	RLQLSNDNRTLTLLS	1942	0.0048	-0.0017	6000'0-	
LSLSCHAAS	2090	GVNLSLSCHAASNPP	1943				
LNLSCHSAS	2091	GANLNLSCHSASNPS	1944				
ASPETHLDM	2092	RLPASPETHLDMLRH	1945				
AHNOVROVP	2093	VLIAHNOVROVPLOR	1946				
LIDTNRSRA	2094	ALTLIDTNRSRACHP	1947				
HHNTHLCF	2095	LALIHHNTHLCFVHT	1948	0.7500	0.0200	0.0330	
LFRNPHOAL	2096	WDQLFRNPHQALLHT	1949	0.0410	-0.0017	-0.000,0	
VDLDDKGCP	2097	HSCVDLDDKGCPAEQ	1950				
YLEDVRLVH	2098	GMSYLEDVRLVHRDL	1951				
IDSECRPRF	2099	CWMIDSECRPRFREL	1952	(0.0001)	-0.0014	0.0028	
AAPOPHPPP	2100	QGGAAPQPHPPAFS	1953				
AAISRKMVE	2101	EFQAAISRKMVELVH	1954				
LHHTLKIGG	2102	VKVLHHTLKIGGEPH	1955				
IGGEPHISY	2103	TLKIGGEPHISYPPL	1956				
AALSRKVAE	2104	EFOAALSRKVAELVH	1957				
LGDPKKLL	2105	EDSILGDPKKLLTQH	1958	0.0130	-0.0014	0.0029	
YKOSOHMTE	2106	MAIYKQSQHMTEVVR	1959				
VEGNLRVEY	2107	LIRVEGNLRVEYLDD	1961				
FTLOIRGRE	2108	GEYFTLQIRGRERFE	1961				

ble XXII. Cross-reactive binding of CEA analog peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Bound
CEA.24	9	LLTFWNPPT	2144	179	1720	67	755	2	2
CEA.24M2V9	9	LMTFWNPPV	2145	4.5	782	7.7	34	3333	3
CEA.24V9	9	LLTFWNPPV	2146	16	307	26	56	952	4
CEA.78	9	Oligyvigt	2147	313	148	106	100	150	5
CEA.78L2V9	9	OLIGYVIGV	2158	9.4	5.9	2.3	21	2.3	5
CEA.233	10	VLYGPDAPTI	2149	128	606	270	804		2
CEA.233V10	10	VLYGPDAPTV	2150	26	430	16	206	952	4
CEA.411	10	VLYGPDDPTI	2151	294	358	476	7400		3
EA.411V10	10	VLYGPDDPTV	2152	161	105	91	2467		3
CEA.569	9	YVCGIONSV	2153	98	358	159	80	181	5
CEA.569L2	ģ	YLCGIONSV	2154	50	24	12	31	3478	4
CEA.589	9	VLYGPDTPI	2155	200	878	53	638		2
CEA.589V9	9	VLYGPDTPV	2156	20	165	91	154	9756	4.
CEA.605	9	YLSGANLNL	2157	28	165	2.4	804		3
CEA.605V9	9	YLSGANLNV	2158	73	13	13	80	1600	4
CEA.687	9	ATVGIMIGV	2159	36	8.8	20	11	0.80	5
CEA.687L2	9	ALVGIMIGV	2160	10	63	31	100	102	5
CEA.691	9	IMIGVLVGV	2161	69	62	13	106	89	5
CEA.691L2	ģ	ILIGVLVGV	2162	22	8.0	3.2	16	160	5

Wild-type peptides presented for reference purposes.
 — indicates binding affinity =10,000nM.



TABLE XXII A A01 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0101 nM
52.0105	11	RVDGNRQIIGY	2163	CEA.72	294.1
52.0109	11	RSDSVILNVLY	2164	CEA.225	47.2
52.0113	11	HSDPVILNVLY	2165	CEA.403	25.8
52.0116	11	RSDPVTLDVLY	2166	CEA.581	7.8
57.0004	9	QQDTPGPAY	2167	CEA.87.D3	56.8
57.0007	9	AADNPPAQY	2168	CEA.261.D3	45.5
57.0008	9	ITDNNSGSY	2169	CEA.289.D3	96.2
57.001	9	VTDNDVGPY	2170	CEA.383.D3	4.1
57.0011	9	PTDSPSYTY	2171	CEA.418.D3	37.9
57.0012	9	TIDPSYTYY	2172	CEA.419.D3	3.1
57.0013	9	AADNPPAQY	2173	CEA.439.D3	44.6
57.0014	9	ITDKNSGLY	2174	CEA.467.D3	11.9
57.0103	10	PTDSPLNTSY	2175	CEA.240.D3	266
57.0104	10	PTDSPSYTYY	2176	CEA.418.D3	1.1
57.0105	10	HTASNPSPQY	2177	CEA.616.T2	131.6
57.0106	10	HSDSNPSPQY	2178	CEA.616.D3	44.6



Table XXII B A03 Analog Peptides

3 XRN	4	က	ო	ო	က	က	ည	က	4	က	c	7
.6801 nM	8.7	7.3	666.7	5714.3	8.6	6.7	2.6	21.6	42.1	2352.9	C	5.3
A*3301 nM ,	557.7	-48333.3	6041.7	-72500	263.6	26363.6	28	4328.4	7631.6	41428.6	100	-/2500
A*3101 nM	187.5	10588.2	11.3	163.6	29	3673.5	25.7	, 720	6	233.8	0000	-36000
A*1101 nM	54.5	6.3	222.2	20	3000	42.9	13.3	54.5	93.8	31.6	0000	206.9
A*0301 nM /	458.3	16.9	343.8	37.9	2340.4	68.8	91.7	17.2	297.3	20.8		1466.7
Source	CEA.241.V2	CEA.241.V2K10	CEA,376.V2	CEA.376.V2K10	CEA.419.V2	CEA.419.V2K10	CEA.420.V2	CEA.420.V2K9	CEA.554.V2	CFA 554 V42K10		CEA.656.K9
SEO ID NO:	2179	2180	TR 2181	2182	2183	2184	2185	2186	2187	2188	2	2189
Segmence	TVSPI NTSYR	TVSPI NTSYK	RVI TI I SVTR	RVI TI I SVTK	TVSPSYTYYR	TVSPSYTYYK	WESYTYYR	IVPSYTYYK	BVI TI FNVTR	DVI TI ENVTK		FVSNLATGK
ΑA	∮⊊	2 5	2 5	2 5	5 5	5 5	2 σ	0	, C	2 5	2	თ
antida	2710	271.02	371.02	371.04	371.05	271.00	271.00	27.1.0.	27.00	27. 4	2	371.13



Table XXIIC A24 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*2401 nM
52.0033	8	IYPNASLL	2190	CEA.101	176.5
52.0038	8	SWFVNGTF	2191	CEA.270	480
52.0137	11	RWCIPWQRLLL	2192	CEA.10	151.9
52.0138	11	PWQRLLLTASL	2193	CEA.14	324.3
52.0141	11	FYTLHVIKSDL	2194	CEA.119	480
52.0142	11	TYLWWVNNQSL	2195	CEA.175	85.7
52.0144	11	TYLWWVNNQSL	2196	CEA.353	46.2
52.0145	11	SYTYYRPGVNL	2197	CEA.423	218.2
52.0146	11	TYYRPGVNLSL	2198	CEA.425	131.9
52.0147	11	TYLWWVNGQSL	2199	CEA.531	92.3
57.0036	9	RYCIPWQRF	2200	CEA.10.Y2F9	190.5
57.0037	9	IYPNASLLF	2201	CEA.101.F9	2.2
57.0038	. 9	LYWVNNQSF	2202	CEA.177.Y2F9	63.2
57.0039	9	LYGPDAPTF	2203	CEA.234.F9	63.2
57.0041	9	TYYRPGVNF	2204	CEA.425.F9 -	52.2
57.0042	9	LYWVNGQSF	2205	CEA.533.Y2F9	15.8
57.0044	9	QYSWRINGF	2206	CEA.624.F9	109.1
57.0045	9	TYACFVSNF	2207	CEA.652.F9	8.6
57.0072	10	RYCIPWQRLF	2208	CEA.10.Y2F10	26.1
57.0073	10	FYNPPTTAKF	2209	CEA.27.Y2F10	181.8
57.0074	10	VYPELPKPSF	2210	CEA.140.F10	106.2
57.0075	10	TYQQSTQELF	2211	CEA.276.Y2	307.7
57.0076	10	VYAEPPKPFF	2212	CEA.318.F10	26.7
57.0077	10	YYRPGVNLSF	2213	CEA.426.F10	10
57.0078	10	OYSWLIDGNF	2214	CEA.446.F10	60
57.0079	10	SYLSGANLNF	2215	CEA.604.F10	10



Table XXIII. Immunogenicity of A2 supermotif-bearing peptides

Peptide	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	Alleles Bound	CTL Peptide ¹ .	CTL Wild-type	CTL
CEA.78	6	QILGYVIGT	2216	313	148	106	100	151	5		0/3	
CEA.354	01	YLWWVNNQSL	2217	56	108	26	487	333	5		1/2	0/1
CEA.569	6	YVCGIQNSV	2218	86	358	159	80	182	2		1/2	0/1
CEA.605	6	YLSGANLNL	2219	28	165	2	804	7	3		2/2	1/2
CEA.687	6	ATVGIMIGV	2220	36	6	20	11	_	5		1/1	1/1
CEA.691	6	IMIGNLVGV	2221	69	62	13	901	68	5		8/8	4/7
CEA.24	6	LLTFWNPPT	2222	179	1720	29	755	: 5	7		0/1	0/1
CFA 24V9	6	LLTFWNPPV	2223	16	307	56	26	952	4	1/1		1/1
CEA.233	2	VLYGPDAPTI	2224	128	909	270	804	1	2		2/4	0/3
CEA.233V10	10	VLYGPDAPTV	2225	76	430	16	506	952	4	3/4	2/2	1/4
CEA.589	6	VLYGPDTPI	2226	200	878	53	638	1	7		Ξ	0/1
CEA.589V9	6	VLYGPDTPV	2227	20	165	91	154	9226	4	2/2	2/2	0/2
CEA.605	6	YLSGANLNL	2228	28	165	2.4	804	:	n		2/2	1/2
CEA 605V9	6	YLSGANLNV	2229	73	13	13	80	1600	4	4/4	3/4	1/4

1) Number of donors yielding a positive response/total tested. 2) -- indicates binding affinity =10,000nM.



Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

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	SEQ ID NO:	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2242	2243	2254	2255	2256	2257	2258	2259	2260
Radiolabeled peptide	Sequence	YTAVVPLVY	FLPSDYFPSV	FLPSDYFPSV	FLPSDYFPSV	FLPSDYFPSV	FLPSDYFPSV	KVFPYALINK	KVFPYALINK	AYIDNYNKF	KVFPYALINK	KVFPYALINK	STLPETYVVRR	FTQAGYPAL	APRTLVYLL	FLKDYQLL	FRYNGLIHR	FPFKYAAAF	FPFKYAAAF	FPFKYAAAF	AEMGKYSFY	FPFKYAAAF	FPFKYAAAF	FPFKYAAAF	QYDDAVYKL	YRHDGGNVL	YRHDGGNVL	SGPSNTYPEI	RGYVFQGL	RGPYRAFVTI	KFNPMKTYI	IPQSLDSYWTSL
Radio	Source	Hu. J chain 102-110	HBVc 18-27 F6->Y	HBVc 18-27 F6->Y	HBVc 18-27 F6->Y	HBVc 18-27 F6->Y	HBVc 18-27 F6->Y	non-natural (A3CONI)	non-natural (A3CON1)	non-natural (A24CON1)	non-natural (A3CON1)	non-natural (A3CON1)	HBVc 141-151 T7->Y	HBV pol 646-654 C4->A	A2 sigal seq. 5-13 (L7->Y)	HIVgp 586-593 Y1->F, Q5->Y	R 60s	non-natural (B35CON2)	non-natural (B35CON2)	non-natural (B35CON2)	EF-1 G6->Y	non-natural (B35CON2)	non-natural (B35CON2)	non-natural (B35CON2)	non-natural (C4CON1)	non-natural (C6CON1)	non-natural (C6CON1)	Adenovirus E1A P7->Y	VSV NP 52-59	HIV-IIIB ENV G4->Y	non-natural (KdCON1)	HBVs 28-39
	Cell line	Steinlin	۲,	P815 (transfected)	FUN	CLA	721.221 (transfected)	GM3107	BVR	KAS116	SPACH	LWAGS	CIR	AMAI	GM3107	Steinlin	1.62	CIR, BVR	TISI	EHM	PITOUT	KAS116	AMAI	KT3	CIR	721.221 transfected	721.221 transfected	EL4	EL4	P815	P815	P815
	Allele	A*0101	A*0201	A*0202	A*0203	A*0206	A*0207			A*2402	A*3101	A*3301	A*6801	A*6802	B*0702	B*0801	B*2705	B*3501	B*3502	B*3503	B*4403		B*5301	B*5401	Cw*0401	Cw*0602	Cw*0702					
	Species Antigen	Human Al		A2	A2	A2	¥2	A3	: IV	A24	A31	A33	A28/68	A28/68	87	B8	B27	B35	B35	B35	B44	B51	B53	B54	Cw4	Cw6	Cw7	Mouse Db	Υ°	۵	Υ ^q	P



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Allele	Cell line		Nautotabeleu peptitue Sequence	SEQ ID NO:
JRB1*0101	TQ5	HA Y307-319	YPKYVKQNTLKLAT	2261
DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY	2262
DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAAAFA	2263
RB1*0301	MAT	MT 65kD Y3-13	YKTIAFDEEARR	2264
DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT	2265
DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA	2266
DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT	2267
ORB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT	2268
DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE	2269
DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE	2270
DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE	1777
DRR1*0901	QIH	Tet. tox. 830-843	QYIKANSKFIGITE	2272
DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE	2273
DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS	2274
DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE	2275
DRB5*0101	GM3107 or L/416.3	Tet. tox. 830-843	QYIKANAKFIGITE	2276
DRB5*0201	1.255.1	HA 307-319	PKYVKQNTLKLAT	7722
DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL	2278
DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT	2279
OA1*0301/DOB1*030	FF	non-natural (ROIV)	YAHAAHAAHAAHAA	2280
	DB27.4	non-natural (ROIV)	YAHAAHAAHAAHAA	2281
	A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2282
	CH-12	HEL 46-61	YNTDGSTDYGILQINSR	. 2283
	LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAA	2284
	91.7	non-natural (ROIV)	YAHAAHAAHAAHAA	2285
	A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK	2286
	CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK	2287



Table XXVI. Crossbinding data of A2 supermotif peptides.

Source	AA	Sequence	SEQ EQ	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
CEA 24	6	LLTFWNPPT	2288	179	1720	<i>L</i> 9	755	:	2
CEA 78	6	OliGYVIGT	2289	313	148	901	100	120	2
CEA 233	01	VLYGPDAPTI	2290	128	909	270	804	:	2
CEA.354	10	YLWWVNNQSL	2291	56	108	56	487	<i>L</i> 9	2
CEA.411	10	VLYGPDDPTI	2292	794	358	476	7400	:	e
CEA.432	6	NLSLSCHAA	2293	455	2867	1449	18500	:	-
CEA.532	10	YLWWVNGQSL	2294	33	331	21	5056	586	4
CEA.569	6	YVCGIQNSV	2295	86	358	159	8	181	S
CEA.589	6	VLYGPDTPI	2296	200	878	53	638	:	7
CEA.605	6	YLSGANLNL	2297	28	165	2.4	804	:	n
CEA.687	6	ATVGIMIGV	2298	36	8.8	70	Ξ	0.80	\$
CEA.690	10	GIMIGVLVGV	2299	4	205	31	142	200	5
CEA.691	6	IMIGVLVGV	2300	69	62	13	106	68	5
CEA.691	10	IMIGVLVGVA	2301	22.7	89	44	726	1509	3

indicates binding affinity =10,000nM.



Table XXVII. Immunogenicity of A2 supermotif peptides

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			SEO ID	A*0201	A*0202	A*0203	A*0206	A*6802	No. A2	71.7 W::14 ft.ii.9	Ę
Source	AA	Sequence	S S	Mn	Mn	Mn	Mn	Mu	Alleles Crossbound	wild-type	Tumor
CEA 78	0	OliGYVIGT	2302	313	148	901	100	151	5	0/3	
CEA.76	, 5	VI WWWNOSI	2303	56	108	76	487	333	8	1/2	70
CEA.334	2 €	ASNOCIONAL	2304	8	358	159	08	182	5	1/2	0/1
CEA.309	^	I VCOIQING V	5	? ;				7	ŗ	277	21
CEA.605	6	YLSGANLNL	2305	78	165	7.4	\$04	: ;	n '	4 :	
CEA 687	6	ATVGIMIGV	2306	36	8.8	20	Ξ	0.80	n	<u>.</u>	<u> </u>
CEA.691	6	IMIGVLVGV	2307	69	62	13	106	83	S	8/8	4/7

1) Number of donors yielding a positive response/total tested. 2) -- indicates binding affinity =10,000nM.



Table XXVIII. Immunogenicity A2 supermotif analog peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide	CTL Wild-type	CTL
CEA.24	6	LLTFWNPPT	2308	179	1720	19	755	- 2	2		0/1	1/0
CFA 24V9	0	LLTFWNPPV	2309	16	307	56	99	952	4	1/1		1/1
CEA 233	\ <u>=</u>	VI.YGPDAPTI	2310	128	909	270	804	1	2		2/4	0/3
CEA 233V10	2	VLYGPDAPTV	2311	56	430	16	206	952	4	3/4	2/2	1/4
CEA 589	: -	VI.VGPDTPI	2312	200	878	53	638	:	7		1/1	0/1
CEA 589V9	۰ ٥	VLYGPDTPV	2313	20	165	16	154	9226	4	2/2	2/2	0/2
CEA 605	6	YI SGANLNL	2314	78	165	2.4	804	:	3		2/2	1/2
CEA 605V9	. 0	YLSGANLNV	2315	73	13	13	80	1600	4	4/4	3/4	1/4

1) Number of donors yielding a positive response/total tested.
2) -- indicates binding affinity =10,000nM.



Table XXIX. DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- reactivity
39.0217	2	RWCIPWQRLLLTASL	2316	CEA.10	8.2	542	357	3
39.0218	3	ORLLLTASLLTFWNP	2317	CEA.16				0
39.0219	2	EVLLLVHNLPOHLFG	2318	CEA.50	2.0	52	53	3
39.0220	3	GREIIYPNASLLION	2319	CEA.97	8.1	484	45	3
39.0221	2	EIIYPNASLLIQNII	2320	CEA.99	14	1154	156	2
39.0222	2	NASLLIONIIONDTG	2321	CEA.104	4546			0
39.0223	3	DTGFYTLHVIKSDLV	2322	CEA.116	69	1731	227	2
39.0224	2	YPELPKPSISSNNSK	2323	CEA.141	5556			0
39.0225	2	KPSISSNNSKPVEDK	2324	CEA.146	2381		7576	0
39.0226	3	YLWWVNNQSLPVSPR	2325	CEA.176	0.59	8.0	42	3
39.0227	3	LWWVNNQSLPVSPRL	2326	CEA.177	217	1552	3049	1
39.0228	2	OYSWFVNGTFOOSTO	2327	CEA.268	192	80	926	3
39.0229	2	DTGLNRTTVTTITVY	2328	CEA.305			2841	0
39.0230	2	KPFITSNNSNPVEDE	2329	CEA.324				0
39.0231	2	NRTLTLLSVTRNDVG	2330	CEA.375	238			1
39.0232	2	OELFISNITEKNSGL	2331	CEA.460		2500		0
39.0233	3	RTTVKTITVSAELPK	2332	CEA.488	455	7031	317	2
39.0234	2	SAELPKPSISSNNSK	2333	CEA.497				0
39.0235	2	LDVLYGPDTPIISPP	2334	CEA.587				0
39.0236	2	TOVLFIAKITPNNNG	2335	CEA.637	61		6579	1
39.0237	2	OVLFIAKITPNNNGT	2336	CEA.638	42	1875		1
39.0238	3	YACFVSNLATGRNNS	2337	CEA.653	208	1667	3571	1
39.0239	2	NNSIVKSITVSASGT	2338	CEA.665	91	25	676	3
39.0239	3	NSIVKSITVSASGTS	2339	CEA.666	78	25	329	3

⁻⁻ indicates binding affinity =10,000nM.



Table XXX DR supertype crossbinding

Peptide	Sequence	SEQ ID NO:	Source	DR1	DR4w4 nM	DR7 nM	DR2w281 nM	DR2w281 DR2w282 DR6w19 nM nM nM	DR6w19 nM	DR5w11 nM	DR8w2 nM	DR147 Degen	Broad Degen (5/8)
	- 10	22.40	OEA 10	8.2	542	357	827		318	1		3	2
39.0717	KWCIPWUKLLLIASL	75-0	CEO.10	1					-	003	400	-	1
39 0219	EVLLLVHNLPOHLFG	2341	CEA.50	2.0	52	53	40	•	0.1	200	400	2	,
30.000	١٠.	2342	CEA.97	8.1	484	45	24	8333	2.9	6897	5904	~	~
25.025	FIIVDNAVI I IONII	2343	CEA 99	14	1154	156	57	:	Ξ	:	:	2	4
39.0221	DECEVER UNIVERSIVE	2344	CEA 116	8	1731	227	206	808	3889	2500	790	7	\$
39.0223	DIOFTILITATION BYOND	37.55	CEA 176	090	0 &	42	110	2105	2.3	29	1065	3	9
39.0226	YLWWVNNQSLFVSFR	240	021.0	20.0		300		1909	5833	370		3	4
39.0228	QYSWFVNGTFQQSTQ	2346	CEA.208	761	00	072		1000	666			c	
10 01	RTTVKTITVSAELPK	2347	CEA.488	455	7031	317	364	1	00/	:	:	7	+
20.020	MNSTVKSTTVSASGT	2348	CEA.665	16	25	9/9	3138	:	51	1	4083	3	4
29.0239	19	2340	CEA.666	78	25	329	3957	:	. 9/	:	2882	3	4
29.0240	2	71.07											

-- indicates binding affinity =10,000nM.



Table XXXI. DR3 binding

7 Peptide	Sequence	SEQ ID NO:	Source	DR3 nM
39.0313	QNIIQNDTGFYTLHV	2350	CEA.110	938
39.0314	LHVIKSDLVNEEATG	2351	CEA.122	2308
39.0315	KSDLVNEEATGQFRV	2352	CEA.126	
39.0316	SDLVNEEATGQFRVY	2353	CEA.127	
39.0317	NEEATGQFRVYPELP	2354	CEA.131	
39.0318	QFRVYPELPKPSISS	2355	CEA.137	
39.0319	AVAFTCEPETQDATY	2356	CEA.162	
39.0320	TASYKCETQNPVSAR	2357	CEA.210	
39.0321	NVLYGPDAPTISPLN	2358	CEA.232	
39.0322	ISPLNTSYRSGENLN	2359	CEA.242	
39.0323	SGSYTCQAHNSDTGL	2360	CEA.294	
39.0324	TITVYAEPPKPFITS	2361	CEA.315	
39.0325	SNPVEDEDAVALTCE	2362	CEA.332	
39.0326	AVALTCEPEIQNTTY	2363	CEA.340	
39.0327	NQSLPVSPRLQLSND	2364	CEA.360	
39.0328	RLQLSNDNRTLTLLS	2365	CEA.368	938
39.0329	ECGIQNELSVDHSDP	2366	CEA.392	
39.0330	ONELSVDHSDPVILN	2367	CEA.396	3659
39.0331	NVLYGPDDPTISPSY	2368	CEA.410	
39.0332	GVNLSLSCHAASNPP	2369	CEA.430	
39.0333	TITVSAELPKPSISS	2370	CEA.493	
39.0334	AVAFTCEPEAQNTTY	2371	CEA.518	
39.0335	SDPVTLDVLYGPDTP	2372	CEA.582	
39.0336	DVLYGPDTPIISPPD	2373	CEA.588	
39.0337	GANLNLSCHSASNPS	2374	CEA.608	

⁻⁻ indicates binding affinity =10,000nM.



Table XXXII. HTLCandidate Epitopes

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Peptide	Sequence	SEQ ID NO:	Motif	Source	DR1 nM	DR4w4 nM	DR7	DR3 nM	DR2w2 B1 nM	DR2w2 B2 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR147 Cross- reactivity	Broad Cross- reactivity (5/8)	DR3 Binder
		١			1				200		910			,		ا
39.0217	RWCIPWORLLLTASL	2375	DR sup	CEA.10	8.7	247	35/	:	/78		318	:		2	٦	
30 0210	FVI I.I VHNI POHLFG	2376	DR sup	CEA.50	2.0	52	53	336	4	:	1.0	588	408	3	7	-
30 0220	GREITYPNASLLION	2377	DR sup	CEA.97	8.1	484	45	1123	24	8333	5.9	2689	5904	3	5	0
30 0313	ONITONDEGEVELHV	2378	DR3	CEA.110	1136	>8182	:	938	298		6.7	:	:	0	2	-
30 0233	DTGFYT! HVIKSDLV	2379	DR sup	CEA.116	69	1731	227		206	800	3889	2500	2067	2.	S	0
39 0726	YLWWYNNOSLPVSPR	2380	DR Sup	CEA.176	09.0	8.0	42	2310	110	2105	2.3	29	1065	3	9	0
39 0328	39 0328 REOLSNDNRTLTLES	2381	DR3	CEA.368	:	>8182	:	938	:	-	729	:	;	٥	-	-

-- indicates binding affinity =10,000nM.

Bronel